PTOPCT Rec's 30 MAY 2001

SEQUENCE LISTING

<110>	Xia, Z Costa, Davin, Lewis,	, Mid , Lau	chael irend	L A ce B											
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Leu G	gt cac ly His 50	tca Ser	gtt Val	gtc Val	gag Glu 55	gcc Ala	att Ile	ggc Gly	act Thr	tcc Ser 60	aat Asn	tcc Ser	acc Thr	tac Tyr	192
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Gly	Ile	Ser	Asp 100	Pro	Asn	Arg	Pro	Arg 105	Ile	Ile	Asp	Asn	Glu 110	Lys	Ala	
	ttt Phe															384
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ttc Phe	ggg	ctt Leu 195	cct Pro	acg Thr	gct Ala	tta Leu	ggc Gly 200	aag Lys	aaa Lys	ttt Phe	tca Ser	ggg Gly 205	att Ile	aaa Lys	aat Asn	624
_	gaa Glu 210	_				_							_			672
	aaa Lys			_		_	_	_		_				-	-	720
	gat Asp															768
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tct Ser																819
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Leu	Ile	Thr	Gly 20	Gly	Ala	Ser	Gly	Ile 25	Gly	Glu	Thr	Thr	Ala 30	Lys	Leu	
Phe	Ser	Gln	His	Gly	Ala	Lys	Val	Ala	Ile	Ala	Asp	Val	Gln	Asp	Glu	

35 45 Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile 135 Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His 150 Ala Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn 200 Glu Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly 215 220 Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly 250 Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser <210> 3 <211> 831 <212> DNA <213> Forsythia x intermedia <220> <221> CDS <222> (1)..(831)

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48

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1				5					10					15			
gga Gly	aaa Lys	gtt Val	gcc Ala 20	ctt Leu	ata Ile	aca Thr	gga Gly	gga Gly 25	gcc Ala	agt Ser	gga Gly	att Ile	gga Gly 30	gaa Glu	acc Thr	96	
	gca Ala															144	
gtc Val	caa Gln 50	gat Asp	gaa Glu	tta Leu	ggt Gly	cac His 55	tca Ser	gtt Val	gtc Val	gag Glu	gcc Ala 60	att Ile	ggc Gly	act Thr	tcc Ser	192	
	tcc Ser															240	
	gcc Ala															288	
	agc Ser															336	
	gaa Glu		_	_		_	_	_		_	_					384	
	ttc Phe 130															432	
	ggc Gly															480	
	tct Ser															528	
	agg Arg															576	
	ttg Leu															624	
	att Ile 210															672	
	ctg Leu															720	
	tat Tyr															768	

245 250 255 ttc att gat gga ggg ttc agc gtc tgc aat tct gta atc aaa gtg ttc Phe Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe 270 260 265 caa tat cca gat tct 831 Gln Tyr Pro Asp Ser 275 <210> 4 <211> 277 <212> PRT <213> Forsythia x intermedia <400> 4 Met Ala Ala Thr Ser Gln Val Leu Thr Ala Ile Ala Arg Arg Leu Glu Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr 20 Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp 100 105 Asn Glu Lys Ala Asp Phe Glu Arg Val Phe Ser Val Asn Val Thr Gly 120 Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Ile Pro Ala Arg 135 Ser Gly Asn Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn 180 190 185 Cys Leu Ser Pro Phe Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser 200 Gly Ile Lys Asn Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly 210

Asn Leu Lys Gly Pro Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala

225 230 235 240 Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu 250 Phe Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser 275 <210> 5 <211> 819 <212> DNA <213> Forsythia x intermedia <220> <221> CDS <222> (1)..(819) atg cag ctt cga act gca atc gca aga agg cta gaa gga aaa gtt gcc 48 Met Gln Leu Arg Thr Ala Ile Ala Arg Arg Leu Glu Gly Lys Val Ala ctt ata aca gga ggc agt gga gtt gga gaa gtc aca gca aaa ctc Leu Ile Thr Gly Gly Ala Ser Gly Val Gly Glu Val Thr Ala Lys Leu 96 20 ttc tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa 144 Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu tta ggt cac tca gtt gtc gag gcc att ggc cct tcc aat tcc acc tac 192 Leu Gly His Ser Val Val Glu Ala Ile Gly Pro Ser Asn Ser Thr Tyr 50 atc cac tgc gat gtt act aat gaa gac ggt gtt aaa aat gcc gtg gac 240 Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp 75 aac aca gtt tca acc tat gga aaa ctg gac att atg ttc aac aat gca 288 Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Asn Asn Ala gga att tet gat eec tae aag eec egg gte ata gae aac gaa aaa gea 336 Gly Ile Ser Asp Pro Tyr Lys Pro Arg Val Ile Asp Asn Glu Lys Ala 105 gac ttt gaa cgc gtt ctc agt gtn aat gtn acc gga gtt ttc cta ttt 384 Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe 120 atg aag cac gca gca cgc att atg gtt cca gca cga aat ggc tgc ata 432 Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile 135 att tcc act gct agt tta agc tca act atg ggt ggt ggt tct tca cat 480 Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His

145		150				155					160	
gct tat tgt Ala Tyr Cys												528
gca gtc gag Ala Val Glu												576
ttc ggg ctt Phe Gly Leu 195												624
gat gta gac Asp Val Asp 210			Ile									672
aca aaa ttg Thr Lys Leu 225												720
agt gat gag Ser Asp Glu												768
ggg ttc agc Gly Phe Ser												816
tct Ser												819
	chia × ir	ntermedi	.a									819
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Asp Phe Glu Arg Val Leu Ser Xaa Asn Xaa Thr Gly Val Phe Leu Phe 125 115 120 Met Lys His Ala Ala Arg Ile Met Val Pro Ala Arg Asn Gly Cys Ile 135 Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Ser Ser His 150 Ala Tyr Cys Gly Ala Lys His Ala Val Leu Gly Leu Thr Arg Asn Leu 170 Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Ser Gly Ile Glu Asn 195 200 205 Asp Val Asp Phe Ala Asn Ala Ile Glu His Ala Gly Asn Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu Phe Leu Ala 225 230 Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly 245 250 Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Met Phe Gln Tyr Pro Asp 265 Ser <210> 7 <211> 831 <212> DNA <213> Forsythia x intermedia <220> <221> CDS <222> (1)..(831) <400> 7 atg gcc agt act tca cag gtt cta act gca atc aca aga agg cta gaa 48 Met Ala Ser Thr Ser Gln Val Leu Thr Ala Ile Thr Arg Arg Leu Glu 10 15 gga aaa gtt gcc ctt ata aca gga gga gcc agt gga att gga gaa ttc 96 Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Phe 20 aca gca aaa ctc ttc tcc caa cat gga gcc aaa gtt gcc att gct gat 144 Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp 35 45 40 gtc caa gat gaa tta ggt cac tca gtt gtc gag gcc atc ggc act tcc Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser 55 60

						_	gat Asp	_			_	-	_	_		240
							tca Ser									288
							gac Asp									336
							cgc Arg 120									384
_			_	_	-		gca Ala	_	_		_			_	_	432
_		_					gct Ala	_	_	_						480
							tgt Cys									528
							ctc Leu									576
_	_	_					gct Ala 200	_			_	_			_	624
							ttg Leu									672
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		_	_	-	_		gca Ala				_				_	768
							gtc Val									816
			gac Asp													831

<210> 8 <211> 277 <212> PRT <213> Forsythia x intermedia

<400> 8

Met Ala Ser Thr Ser Gln Val Leu Thr Ala Ile Thr Arg Arg Leu Glu $1 5 10 1^{\cdot 5}$

Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Phe 20 25 30

Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp $35 \hspace{1cm} 40 \hspace{1cm} 45$

Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser 50 55 60

Asn Ser Ile Tyr Ile His Cys Asp Val Thr Asn Glu Asp Asp Val Lys 65 70 75 80

Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met 85 90 95

Phe Asn Asn Ala Gly Ile Ala Asp Pro Asn Lys Pro Arg Ile Val Asp 100 105 110

Asn Glu Lys Ala Asp Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly 115 120 125

Val Phe Leu Cys Met Lys His Ala Ala Arg Val Met Val Pro Ala Arg 130 135 140

Ser Gly Ser Ile Ile Ser Thr Ala Ser Val Ser Ser Thr Ile Gly Gly 145 150 155 160

Ala Ala Ser His Ala Tyr Cys Cys Ser Lys His Ala Val Leu Gly Leu 165 170 175

Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn 180 185 190

Cys Leu Ala Pro Tyr Ala Leu Ala Thr Pro Leu Ala Lys Lys Phe Val 195 200 205

Gly Leu Glu Asn Asp Glu Asp Leu Glu Asn Ala Met Ser Leu Met Gly 210 215 220

Asn Leu Lys Gly Thr Asn Leu Lys Ala Glu Asp Val Ala Asn Ala Ala 225 230 235 240

Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu 245 250 255

Phe Ile Asp Gly Gly Phe Ser Val Tyr Asn Ser Al'a Ile Lys Met Phe 260 265 270

Gln Tyr Pro Asp Thr 275

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	_	_		ata Ile				-	_		-		_	-		96
				tcc Ser												144
caa Gln	gat Asp 50	gaa Glu	tta Leu	ggt Gly	cac His	tca Ser 55	gtt Val	gtc Val	gag Glu	gcc Ala	att Ile 60	ggc Gly	ctt Leu	tcc Ser	aat Asn	192
				cac His												240
				aca Thr 85												288
		_		att Ile		_			_			-		-		336
				ttt Phe												384
Phe				aag Lys												432
				tcc Ser												480
				tat Tyr 165												528
				gtc Val												576
				ggg												624

att gaa aat Ile Glu Asn 210			Ala A			u Arg				672
ctg aaa ggt Leu Lys Gly 225										720
ttt ctg gct Phe Leu Ala								_		768
atc gat gga Ile Asp Gly			. Cys A							816
tat cca gac Tyr Pro Asp 275										828
<210> 10 <211> 276 <212> PRT <213> Forsy	thia x in	ntermedi	.a							
<400> 10	Cor Cln	Iou Arc	. ሞЬ∽ ሽ	la Pho	70 1 2 7 2 T	a Ara	Ton	Clu	Clu	
Met Ala Thr 1	5	rea Ard	Int A	10	Ald Al	g Arg	Leu	15	сту	
Lys Val Ala	Leu Ile 20	Thr Gly		la Ser 25	Gly Va	l Gly	Glu 30	Val	Thr	
Ala Lys Leu 35	Phe Ser	Gln His	Gly A 40	la Lys	Val Al	a Ile 45	Ala	Asp	Val	
Gln Asp Glu 50	Leu Gly	His Ser		al Glu		e Gly	Leu	Ser	Asn	
Ser Thr Tyr 65	Ile His	Cys Asp 70	Val T	hr Asn	Glu As 75	p Gly	Val	Lys	Asn 80	
Ala Val Asp	Asn Thr 85	Val Sei	Thr T	yr Gly 90	Lys Le	u Asp	Ile	Met 95	Phe	
Asn Asn Ala	Gly Ile 100	Ser Asp	_	yr Lys .05	Pro Ar	g Val	Ile 110	Asp	Asn	
Glu Lys Ala 115	Asp Phe	Glu Aro	Val L 120	eu Ser	Val As	n Val 125	Thr	Gly	Val	
Phe Leu Phe 130	Met Lys	His Ala		rg Ile	Met Va	_	Ala	Arg	Ser	
Gly Cys Ile 145	Ile Ser	Thr Ala	Ser L	eu Ser	Ser Th	r Met	Gly	Gly	Gly 160	
		130								

Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys 180 185 190 Leu Ser Pro Phe Gly Leu Pro Thr Pro Leu Ala Lys Lys Phe Thr Gly Ile Glu Asn Asp Glu Asp Leu Ala Asn Gly Ile Glu Arg Ala Gly Asn 215 Leu Lys Gly Thr Lys Leu Arg Ile Glu Asp Val Ala Asn Ala Ala Leu 230 Phe Leu Ala Ser Asp Glu Ala Gln Tyr Val Ser Gly Gln Asn Leu Phe Ile Asp Gly Gly Phe Ser Val Cys Asn Ser Ala Ile Lys Leu Phe Gln 260 Tyr Pro Asp Ser 275 <210> 11 <211> 21 <212> PRT <213> Forsythia x intermedia <220> <221> PEPTIDE <222> (1)..(21) <223> N-terminal peptide of F. intermedia secoisolariciresinol protein wherein Xaa at positions 3, 12 and 20 represents an unidentified amino acid residue <400> 11 Gln Val Xaa Thr Ala Ile Ala Arg Asp Leu Glu Xaa Lys Val Ala Leu Ile Thr Gly Xaa Ala <210> 12 <211> 17 <212> PRT <213> Forsythia x intermedia <400> 12 Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys <210> 13 <211> 15 <212> PRT

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<213> Forsythia x intermedia
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<223> Description of Artificial Sequence:
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<220>
<221> misc_feature
<222> (1)..(20)
<223> PCR primer wherein n at positions 3, 9, 15 and 18
      represents inosine
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                                                                    20
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<210> 15
<211> 20
<212> DNA
<213> Artificial Sequence
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<220>
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      represents inosine
<400> 15
congorting araacatdat
                                                                    20
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<213> Artificial Sequence
<223> Description of Artificial Sequence:
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<223> PCR primer wherein n at positions 3 and 9
      represents inosine
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<210> 20

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ata aca gga gga gcc agt gga att gga gaa acc aca gca aaa ctc ttc
                                                                    96
Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe
tcc caa cat gga gcc aaa gtt gcc att gct gat gtc caa gat gaa tta
                                                                    144
Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu
                             40
ggt cac tca gtt gtc gag gcc att ggc act tcc aat tcc acc tac atc
                                                                    192
Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile
                         55
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	gat Asp														240
	tca Ser														288
	gat Asp					_			_		_		_	_	336
_	cgc Arg 115	-		_	-		_			_			_	_	384
	gca Ala														432
	gct Ala														480
	ggt Gly														528
	ctc Leu														576
	cct Pro 195	-	-			_								_	624
	ttt Phe														672
	aat Asn	_	_	_	-	_		_	_			_	_	_	720
	gca Ala														768
	gtc Val														816

<210> 23 <211> 272 <212> PRT <213> Forsythia x intermedia

Gln Leu Arg Thr Ala Phe Ala Arg Arg Leu Glu Gly Lys Val Ala Leu Ile Thr Gly Gly Ala Ser Gly Ile Gly Glu Thr Thr Ala Lys Leu Phe Ser Gln His Gly Ala Lys Val Ala Ile Ala Asp Val Gln Asp Glu Leu Gly His Ser Val Val Glu Ala Ile Gly Thr Ser Asn Ser Thr Tyr Ile His Cys Asp Val Thr Asn Glu Asp Gly Val Lys Asn Ala Val Asp Asn Thr Val Ser Thr Tyr Gly Lys Leu Asp Ile Met Phe Ser Asn Ala Gly Ile Ser Asp Pro Asn Arg Pro Arg Ile Ile Asp Asn Glu Lys Ala Asp 100 105 110 Phe Glu Arg Val Leu Ser Val Asn Val Thr Gly Val Phe Leu Cys Met 120 Lys His Ala Ala Arg Val Met Ile Pro Ala Arg Ser Gly Asn Ile Ile Ser Thr Ala Ser Leu Ser Ser Thr Met Gly Gly Gly Ser Ser His Ala Tyr Cys Gly Ser Lys His Ala Val Leu Ala Leu Thr Arg Asn Leu Ala Val Glu Leu Gly Gln Phe Gly Ile Arg Val Asn Cys Leu Ser Pro Phe 180 190 Gly Leu Pro Thr Ala Leu Gly Lys Lys Phe Ser Gly Ile Lys Asn Glu 200 Glu Glu Phe Glu Asn Val Ile Asn Phe Ala Gly Asn Leu Lys Gly Pro 215 Lys Phe Asn Val Glu Asp Val Ala Asn Ala Ala Leu Tyr Leu Ala Ser Asp Glu Ala Lys Tyr Val Ser Gly His Asn Leu Phe Ile Asp Gly Gly 250 Phe Ser Val Cys Asn Ser Val Ile Lys Val Phe Gln Tyr Pro Asp Ser

265

260

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<220>

<223> Description of Artificial Sequence:
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